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1 TCAAATTTT CTCCAGTTCT AAATATCCGG AACCTCTTG GGATGCCATT

51 GCCCATCTAT CTGTAATTTA TTGACGAAAT AGACGAAAAG GAAGGTGGCT

101 CCTATAAAGC ACATCATTGC GATAACAGAA AGGCCATTGT TGAAGATACC

151 TCTGCTGACA TTGGTCCCCA AGTGGAAGCA CCACCCCATG AGGAGCACCG

201 TGGAGTAAGA AGACGTTCTGA GCCACGTCGA AAAAGCAAGT GTGTTGATGT

251 AGTATCTCCA TTGACGTAAG GGATGACGCA CAATCCAAC TCCATCGCA

301 AGACCATTGC TCTATATAAG AAAGTTAATA TCATTTGAG TGGCCACGCT

351 G [SEQ ID NO:2]

FIGURE 2